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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 12:56:11 : search time 3039.87 seconds
        (without alignments) 19183.272 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atctttgttcagttaccc. .... ctttgtgcctccatgtca 6169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Word size : 8

Total number of hits satisfying chosen parameters: 20439225
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
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38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
43: gb_est43:*
44: em_esthnum0:*
45: em_esthnum1:*
46: em_esthnum2:*
47: em_esthnum13:*
48: em_esthnum4:*
49: em_esthnum15:*
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52: em_esthnum1:*
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114: em_estro45:*
115: em_estro46:*
116: em_estro47:*

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200: em_gss_hum7: *
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204: em_gss_inv2: *
205: em_gss_inv3: *
206: em_gss_other: *
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208: em_gss_p102: *
209: em_gss_p103: *
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248: gb_gss31: *
249: gb_gss32: *
250: gb_gss33: *
251: gb_gss34: *
252: em_gss_inv4: *
253: em_gss_r006: *
254: em_gss_r007: *
255: em_gss_r008: *
256: gb_gss35: *
257: gb_gss36: *
258: gb_gss37: *

```

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
tel: 301 402 3452

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	469	7.6	469	168	BF725009	BF725009 bx11a12.y
2	429	7.0	429	168	BF726094	BF726094 bx23h10.y
3	132	2.1	188	188	R95491	R95491 CBS-670 Sub
4	104	1.7	593	122	AW954907	AW954907 EST36697
5	65	1.1	420	229	AQ526246	AQ526246 HS_53309_B
6	58	0.9	273	19	AJ348766	AJ348766 tad5a04.x
7	57	0.9	250	118	AW591614	AW591614 xx135902.x
8	56	0.9	415	188	R88218	R88218 yqf5a05.r1
9	56	0.9	465	228	AQ390434	AQ390434 CTTB1-EL-
10	56	0.9	483	110	AW007449	AW007449 wts5h07.x
11	56	0.9	486	224	AQ134263	AQ134263 HS_3047_B
12	56	0.9	519	19	AQ952388	AQ952388 EST374461
13	56	0.9	525	110	AW024656	AW024656 w778h05.x
14	55	0.9	340	110	AV761433	AV761433 AV761433
15	55	0.9	430	164	AJ143811	BB143811 M00-HT016
16	55	0.9	447	1	AQ055402	AA055402_z17e10.5
17	55	0.9	578	105	AL038533	AL038533 DKPZP56E
18	55	0.9	879	232	AQ738799	AQ738799 HS_5386_B
19	54	0.9	459	228	AQ040412	AQ404012 HS_53070_B
20	53	0.9	350	5	AA318316	AA318316 EST30383
21	53	0.9	340	110	AQ1953189	AQ1953189 bbs465p6
22	53	0.9	528	233	AQ784890	AQ784890 HS_3251_A
23	52	0.8	152	8	AA541310	AA41310 n17b06.s
24	52	0.8	204	232	AQ78330	AA78330 EST91192
25	52	0.8	315	150	BF529627	BF529627 6020043852
26	52	0.8	375	13	AA916366	AA916366 og79b12.s
27	52	0.8	399	191	Z30245	Z30245 HHEP028 AtR
28	52	0.8	457	10	AA653459	AA653459 ag66cc11.s
29	52	0.8	552	9	AA594229	AA594229 nn29105.s
30	52	0.8	229	229	AQ487554	AQ487554 RCT-11-2
31	52	0.8	576	104	AJ179101	AJ179101 w770e01.x
32	51	0.8	376	114	AW018189	AW018189 x184d02.x
33	51	0.8	377	2	AA132947	AA132947 zo19608.s
34	51	0.8	437	2	AA131083	AA131083 201606.s
35	51	0.8	465	24	AJ132596	AJ132596 zo19608.x
36	50	0.8	389	230	AQ544057	AQ544057 RCT-11-3
37	50	0.8	410	32	AV660235	AV660235 AV660235
38	49	0.8	149	169	BF773353	BF773353 CM1-IT004
39	49	0.8	208	224	AQ108180	AQ108180 CIT-HP-2
40	49	0.8	312	122	AW897746	AW897746 RCI-NN006
41	49	0.8	319	150	BF530611	BF530611 6020071889
42	49	0.8	331	188	AJ445373	AJ445373 t124e08.x
43	49	0.8	331	188	T07225	T07225 EST05114 Fe
44	49	0.8	360	245	A2515814	A2515814 RPI-11-1
45	49	0.8	362	169	BF773297	BF773297 CM3-IT004

ALIGNMENTS

Query Match 7.6%; Score 469; DB 168; Length 469;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Origin

QY 5273 caccatccaggagccctccacacagcaggagcggatctccaggatccacaaaggctc 532

QY 5273 caccatccaggagccctccacacagcaggagcggatctccaggatccacaaaggctc 532

Db 1 CACCCATCCAGCACCTCTCAGCACAGCAGCAGCAGCTCCAGGAGCCCTCACCAAGCCCTC 60

QY 5333 tcaatcgggttcttctgtgcacgtgtgcacgtttggcttagatgcacatgtgtca 5392

Db 61 TGCATATGAGTTCTCTGAGCTGCAGCTTGCCGAGATGCCACCTGCTCA 120

QY 5393 gctctgtgtcttctggcttccatgtgtggatgtggggccaggacagtcgtcaggaa 5452

Db 121 GCGCGTCGCTCTGGCTGCTGGTGGATGTTGGGGCCAGACGTCAGCTCAGGA 180

QY 5453 ggccaatggaccagggtggccggccggatgtatccatgtgtggccatccatgt 5512

Db 181 GGCGCHATGACAGAGTGGCGCATGCGTACCTGTCAGTGCGCCAGCCAGTGA 240

QY 5513 cagtcggccaggatggccggccggatgtatccatgtgtggccatccatgt 5572

Db 241 CAGCGCCAGAGCAGAGCAGCCAGCTGACTCTGCTCCCTGGAGACCTCT 300

QY 5573 caccacactttagacccatggggccacaaaggctcgtatccatgtgtggccatccatgt 5632

Db 301 CACCCACGCTTAGCCACCAAGCTGACTCTGCTCCCTGGAGACCTCT 360

QY 5633 ccaccaatggaccagggtggccggccggatgtatccatgtgtggccatccatgt 5692

Db 361 CCACCAATGACCTTGGACCCAGGCTGGAGACCCAGGGCTGGAGCAG 420

QY 5693 ggactgtggccacccatggggccggccggatgtatccatgtgtggccatccatgt 5741

Db 421 GGACCTGGCCACCTGAGCCGGGAGGGCAGCACTGAGAACCAAAC 469

RESULT 1

BF725009 BF725009 469 bp mRNA EST 05-JAN-2001

DEFINITION bx11a12.y1 Human iris cDNA (un-normalized, unamplified): BX Homo

LOCUS Bx11a12.y1 Human iris cDNA (un-normalized, unamplified): BX Homo

DEFINITION Bx11a12.y1 Human iris cDNA clone bx11a12 5', mRNA sequence.

ACCESSION BF725009

VERSION BF725009.1 GI:12040920

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 469)

AUTHORS Wistow, G.J., Bernstein, S., Behar, A. and Smith, D.

TITLE INVEST: EST analysis and bioinformatics for ocular genomics

JOURNAL COMMENT Contact: Wistow G

Db	101	ACAGTCAGTCTGGAGAAGAGAGGAGGACTAATGGCAAGAAATGAGAATCTGGCCAA	160
Oy	5839	99aggttggaaa	5850
Db	161	GGAGTTGGAA	172
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AW954907			
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ACCESSION			EST
VERSION			01-JUN-2000
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SOURCE			Human.
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			Heede, P., Oi, R., Abernathy, K., Dharam, S., Gaspar, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
JOURNAL			Unpublished (2000)
COMMENT			Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
BASE COUNT	151	a 142 c 180 g 120 t	
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		/clone_lib="MAGE I sequences, MAGC"	
		/note="Vector: pBluescriptSKn"	
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		Indices 0;	Gaps 0;
BASE COUNT			
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Best Local Similarity		1.1%	Score 65; DB 229; Length 420;
Matches		65;	Conservative 0; Mismatches 0;
		Indels 0;	Gaps 0;
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity		1.00%	Score 9606; DB 100; Length 593;
Matches		104;	Conservative 0; Mismatches 0;
		Indices 0;	Gaps 0;
BASE COUNT			
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5837		caggagggttggaaagcggccggggatggatggaaaggcttggccca	5896
Oy			
Db		42 CAGGGAGTTGAAAGCAGCAGCAGGAGGAGCAAGCTAGAAGGGCCAGTGCCCCA	101
RESULT	5		
A0526246/C			
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COMMENT			
RESULT	6		
A1348766			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
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JOURNAL			
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COMMENT			
RESULT	6		
A1348766			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS</			

RESULT	9	0.9%; Score 56; DB 188; Length 415;	ORGANISM	Homo sapiens
LOCUS	AQ390434	465 bp DNA GSS 06-MAR-1999	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DEFINITION	CITB1-El-2554E19.TR CITB1-El	Homo sapiens genomic clone 2554E19, DNA sequence.	AUTHORS	1 (bases 1 to 483) NCI-NCAP http://www.ncbi.nlm.nih.gov/ncicgap.
ACCESSION	AQ390434		TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
VERSION	AQ390434.1	GI:4361457	JOURNAL	Unpublished (1997)
KEYWORDS	GSS, human.	COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgraphs-r@mail.nih.gov
SOURCE			Life Technologies catalog #: 11548-013	
ORGANISM	Homo sapiens		DNA Sequencing by: Washington University Genome Sequencing Center	
			Clone distribution: NCI-NCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/IMAGE/image.html	
REFERENCE			Insert Length: 1365 Std Error: 0.00	
AUTHORS			Seq primer: -40UP from Gibco	
TITLE			High quality sequence stop: 412.	
JOURNAL			Location/Qualifiers	
COMMENT			1. . 483	
			/organism="Homo sapiens"	
			/db_xref="taxon:9606"	
			/clone="IMAGE:2511421"	
			/tissue_type="adenocarcinoma"	
			/clone_lib="NCI-NCAP_Parl"	
			/lab_host="DRI0B"	
			/note="Organ: pancreas; Vector: PCMV-SP076; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dR; Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"	
FEATURES			BASE COUNT	140 a 99 c 94 g 150 t
source			ORIGIN	
FEATURES		Query Match 0.9%; Score 56; DB 110; Length 483;	RESULT	11
source		Best Local Similarity 100.0%; Pred. No. 9.6e-15; Mismatches 0; Indels 0; Gaps 0;	LOCUS	AQ134263
		Matches 56; Conservative 0; Gaps 0; Indels 0; Gaps 0;	DEFINITION	486 bp DNA GSS 23-SEP-1998
			ACCESSION	HS:3047_B1_F02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate:3047 Col=3 Row=L, DNA sequence.
			VERSION	AQ134263
			Db	365 GCTCACTGCACCTGTGCCAGGTCAAGCATTCCTGCTCACCTCCG 420
BASE COUNT			ORGANISM	Homo sapiens
ORIGIN			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
			AUTHORS	1 (bases 1 to 483) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
			TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
			JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
			MEDLINE	9980589
			COMMENT	Contact: Mahairas, G.G., Wallace, J.C., Hood, L.
RESULT	10			High Throughput Sequencing Center
LOCUS	AW007449	483 bp mRNA EST 09-MAR-2000		401 Queen Anne Avenue North, Seattle, WA 98109, USA
DEFINITION	W55507_x1 NCI_CCRP_Pan1 Homo sapiens cDNA clone IMAGE:2511421 3'			Tel: (206) 616-3618
	Similar to contains Alu repetitive element; contains element MER18 repetitive element ; mRNA sequence.			Fax: (206) 616-3687
ACCESSION	AW007449			Email: jwallace@u.washington.edu
VERSION	AW007449.1	GI:5056227		Sequence Tagged Connector
KEYWORDS	EST.			Plate: 3047 row: L column: 3
SOURCE	human.			Class: BAC ends

FEATURES	High quality sequence stop: 486.
source	location/Qualifiers
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	/organism="Homo sapiens"
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	/clone="Plate3047 Col=3 Row=L"
	/sex="male"
	/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT	98 a 126 c 102 g 157 t 3 others
ORIGIN	
Query Match	0.9%; Score 56; DB 224; Length 486;
Best Local Similarity	100.0%; Pred. No. 9.5e-15;
Matches	56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1327 gtcactgcaacctctgcctccaaatccatcttcgttcaggatccgg 1382
Db	GCTCACTGCAACCTGCCCTCCAGGTCAAGCAATTCTCTGTCAGCCTCCG 221
RESULT	12
AW962388/c	
LOCUS	AW962388 519 bp mRNA EST 01-JUN-2000
DEFINITION	EST74461 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW962388
VERSION	AW962388.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 519)
AUTHORS	Hegde, P., Oi, R., Aherna, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: Johnq@igr.org Place: 174
FEATURES	Seq primer: Reverse.
source	Location/Qualifiers
	1. .519
	/organism="Homo sapiens"
	/ab_xref="taxon:9606"
	/clone="1b" "MAGE resequences, MAGG"
	/note="Vector: pBluescriptSKin"
BASE COUNT	147 a 125 c 132 g 115 t
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Query Match	0.9%; Score 56; DB 110; Length 525;
Best Local Similarity	100.0%; Pred. No. 9.5e-15;
Matches	56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1327 gtcactgcaacctctgcctccaaatccatcttcgttcaggatccgg 1382
Db	GCTCACTGCAACCTGCCCTCCAGGTCAAGCAATTCTCTGTCAGCCTCCG 417
RESULT	14
AW761433/c	
LOCUS	AV761433 340 bp mRNA EST 19-OCT-2000
DEFINITION	MDS Homo sapiens cDNA clone MDSBEA08 5', mRNA sequence.
ACCESSION	AV761433
VERSION	AV761433.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 340)
AUTHORS	Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tui, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Zhang, H., Chen, S., Han, Z., and Chen, Z.
TITLE	Homo sapiens cDNA MPS clones
JOURNAL	Unpublished (2000)

COMMENT

contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@cgic.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

1. .340

/organism="Homo sapiens"

/db_xref="Taxon:9606"

/clone_id="MDSRA08"

/clone.lib="MDS"

/tissue_type="Bone marrow"

/cell_type="CD34+ hematopoietic stem/progenitor cell"

/lab_host="BM25.8"

/note="Vector: pTRIPEx2; Site_1: sf1IA; Site_2: sf1B"

BASE COUNT

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96 g

61 t

96 t

ORIGIN

BASE COUNT

85 a

121 c

103 g

121 t

ORIGIN

1

/note="Organ: head-neck; Vector: pUC18; Site_1: sf1AI;

Site_2: Smart; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent Application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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